P09 #2
3/7/2002

Serial Number: 09/913,756   ENTERED

CRF Processing Dat: 3/7/2002
Edited by: _____
Verified by: _____ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII

- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- ☐ Edited a format error in the Current Application Data section, specifically:
  _____

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by th applicant was ☐ the prior application data; or ☐ other _____.

- ☐ Added the mandatory heading and subheadings for "Current Application Data".

- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
  _____

- ☑ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: *12*
  _____

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line.   SEQ ID NO's edited:
  _____

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- ☐ Inserted colons after headings/subheadings. Headings edited included:
  _____

- ☐ Deleted extra, invalid, headings used by an applicant, specifically:
  _____

- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

- ☐ Inserted mandatory headings, specifically: _____

- ☐ Corrected an obvious error in the response, specifically:
  _____

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

- ☐ Corrected an error in the Number of Sequences field, specifically:
  _____

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- ☑ Other: *Seq 16 corrected amino acid nos:*
  _____
  _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PCT09

RAW SEQUENCE LISTING   DATE: 03/07/2002
PATENT APPLICATION: US/09/913,756   TIME: 18:40:43

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\03072002\I913756.raw

```
 3 <110> APPLICANT: Chiari, Rita
 4        Coulie, Pierre
 5        Boon-Falleur, Thierry
 7 <120> TITLE OF INVENTION: TYROSINE KINASE RECEPTOR EphA3 ANTIGENIC PEPTIDES
 9 <130> FILE REFERENCE: L0461/7121
11 <140> CURRENT APPLICATION NUMBER: US 09/913,756
12 <141> CURRENT FILING DATE: 2000-02-18
14 <150> PRIOR APPLICATION NUMBER: US 60/121,170
15 <151> PRIOR FILING DATE: 1999-02-22
17 <150> PRIOR APPLICATION NUMBER: US 60/158,566
18 <151> PRIOR FILING DATE: 1999-10-08
20 <160> NUMBER OF SEQ ID NOS: 63
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 43
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial sequence
30 <220> FEATURE:
31 <221> NAME/KEY: primer_bind
32 <222> LOCATION: 1..43
33 <223> OTHER INFORMATION: synthetic oligo(dT) primer
35 <220> FEATURE:
36 <221> NAME/KEY: unsure
37 <222> LOCATION: 43..43
38 <223> OTHER INFORMATION: n = a, c, g or t
40 <400> SEQUENCE: 1
41  ataagaatgc ggccgctaaa ctattttttt tttttttttt tvn                    43
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 3149
46 <212> TYPE: DNA
47 <213> ORGANISM: Homo sapiens
49 <220> FEATURE:
50 <221> NAME/KEY: CDS
51 <222> LOCATION: 101..3052
53 <400> SEQUENCE: 2
54  ccatggatgg taacttctcc agcaatcaga gcgctccccc tcacatcagt ggcatgcttc    60
55  atggagatat gctcctctca ctgccctctg caccagcaac atg gat tgt cag ctc   115
56                                                 Met Asp Cys Gln Leu
57                                                 1               5
59  tcc atc ctc ctc ctt ctc agc tgc tct gtt ctc gac agc ttc ggg gaa   163
60  Ser Ile Leu Leu Leu Leu Ser Cys Ser Val Leu Asp Ser Phe Gly Glu
61                  10              15              20
63  ctg att ccg cag cct tcc aat gaa gtc aat cta ctg gat tca aaa aca   211
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64  Leu Ile Pro Gln Pro Ser Asn Glu Val Asn Leu Leu Asp Ser Lys Thr
65              25              30              35
67  att caa ggg gag ctg ggc tgg atc tct tat cca tca cat ggg tgg gaa    259
68  Ile Gln Gly Glu Leu Gly Trp Ile Ser Tyr Pro Ser His Gly Trp Glu
69              40              45              50
71  gag atc agt ggt gtg gat gaa cat tac aca ccc atc agg act tac cag    307
72  Glu Ile Ser Gly Val Asp Glu His Tyr Thr Pro Ile Arg Thr Tyr Gln
73              55              60              65
75  gtg tgc aat gtc atg gac cac agt caa aac aat tgg ctg aga aca aac    355
76  Val Cys Asn Val Met Asp His Ser Gln Asn Asn Trp Leu Arg Thr Asn
77  70              75              80              85
79  tgg gtc ccc agg aac tca gct cag aag att tat gtg gag ctc aag ttc    403
80  Trp Val Pro Arg Asn Ser Ala Gln Lys Ile Tyr Val Glu Leu Lys Phe
81              90              95              100
83  act cta cga gac tgc aat agc att cca ttg gtt tta gga act tgc aag    451
84  Thr Leu Arg Asp Cys Asn Ser Ile Pro Leu Val Leu Gly Thr Cys Lys
85              105             110             115
87  gag aca ttc aac ctg tac tac atg gag tct gat gat gat cat ggg gtg    499
88  Glu Thr Phe Asn Leu Tyr Tyr Met Glu Ser Asp Asp Asp His Gly Val
89              120             125             130
91  aaa ttt cga gag cat cag ttt aca aag att gac acc att gca gct gat    547
92  Lys Phe Arg Glu His Gln Phe Thr Lys Ile Asp Thr Ile Ala Ala Asp
93              135             140             145
95  gaa agt ttc act caa atg gat ctt ggg gac cgt att ctg aag ctc aac    595
96  Glu Ser Phe Thr Gln Met Asp Leu Gly Asp Arg Ile Leu Lys Leu Asn
97  150             155             160             165
99  act gag att aga gaa gta ggt cct gtc aac aag aag gga ttt tat ttg    643
100  Thr Glu Ile Arg Glu Val Gly Pro Val Asn Lys Lys Gly Phe Tyr Leu
101             170             175             180
103  gca ttt caa gat gtt ggt gct tgt gtt gcc ttg gtg tct gtg aga gta   691
104  Ala Phe Gln Asp Val Gly Ala Cys Val Ala Leu Val Ser Val Arg Val
105             185             190             195
107  tac ttc aaa aag tgc cca ttt aca gtg aag aat ctg gct atg ttt cca   739
108  Tyr Phe Lys Lys Cys Pro Phe Thr Val Lys Asn Leu Ala Met Phe Pro
109             200             205             210
111  gac acg gta ccc atg gac tcc cag tcc ctg gtg gag gtt aga ggg tct   787
112  Asp Thr Val Pro Met Asp Ser Gln Ser Leu Val Glu Val Arg Gly Ser
113             215             220             225
115  tgt gtc aac aat tct aag gag gaa gat cct cca agg atg tac tgc agt    835
116  Cys Val Asn Asn Ser Lys Glu Glu Asp Pro Pro Arg Met Tyr Cys Ser
117  230             235             240             245
119  aca gaa ggc gaa tgg ctt gta ccc att ggc aag tgt tcc tgc aat gct   883
120  Thr Glu Gly Glu Trp Leu Val Pro Ile Gly Lys Cys Ser Cys Asn Ala
121             250             255             260
123  ggc tat gaa gaa aga ggt ttt atg tgc caa gct tgt cga cca ggt ttc    931
124  Gly Tyr Glu Glu Arg Gly Phe Met Cys Gln Ala Cys Arg Pro Gly Phe
125             265             270             275
127  tac aag gca ttg gat ggt aat atg aag tgt gct aag tgc ccg cct cac    979
128  Tyr Lys Ala Leu Asp Gly Asn Met Lys Cys Ala Lys Cys Pro Pro His
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129         280                   285                   290
131   agt tct act cag gaa gat ggt tca atg aac tgc agg tgt gag aat aat     1027
132   Ser Ser Thr Gln Glu Asp Gly Ser Met Asn Cys Arg Cys Glu Asn Asn
133         295                   300                   305
135   tac ttc cgg gca gac aaa gac cct cca tcc atg gct tgt acc cga cct     1075
136   Tyr Phe Arg Ala Asp Lys Asp Pro Pro Ser Met Ala Cys Thr Arg Pro
137   310                   315                   320                   325
139   cca tct tca cca aga aat gtt atc tct aat ata aac gag acc tca gtt     1123
140   Pro Ser Ser Pro Arg Asn Val Ile Ser Asn Ile Asn Glu Thr Ser Val
141         330                   335                   340
143   atc ctg gac tgg agt tgg ccc ctg gac aca gga ggc cgg aaa gat gtt     1171
144   Ile Leu Asp Trp Ser Trp Pro Leu Asp Thr Gly Gly Arg Lys Asp Val
145         345                   350                   355
147   acc ttc aac atc ata tgt aaa aaa tgt ggg tgg aat ata aaa cag tgt     1219
148   Thr Phe Asn Ile Ile Cys Lys Lys Cys Gly Trp Asn Ile Lys Gln Cys
149         360                   365                   370
151   gag cca tgc agc cca aat gtc cgc ttc ctc cct cga cag ttt gga ctc     1267
152   Glu Pro Cys Ser Pro Asn Val Arg Phe Leu Pro Arg Gln Phe Gly Leu
153         375                   380                   385
155   acc aac acc acg gtg aca gtg aca gac ctt ctg gca cat act aac tac     1315
156   Thr Asn Thr Thr Val Thr Val Thr Asp Leu Leu Ala His Thr Asn Tyr
157   390                   395                   400                   405
159   acc ttt gag att gat gcc gtt aat ggg gtg tca gag ctg agc tcc cca     1363
160   Thr Phe Glu Ile Asp Ala Val Asn Gly Val Ser Glu Leu Ser Ser Pro
161         410                   415                   420
163   cca aga cag ttt gct gcg gtc agc atc aca act aat cag gct gct cca     1411
164   Pro Arg Gln Phe Ala Ala Val Ser Ile Thr Thr Asn Gln Ala Ala Pro
165         425                   430                   435
167   tca cct gtc ctg acg att aag aaa gat cgg acc tcc aga aat agc atc     1459
168   Ser Pro Val Leu Thr Ile Lys Lys Asp Arg Thr Ser Arg Asn Ser Ile
169         440                   445                   450
171   tct ttg tcc tgg caa gaa cct gaa cat cct aat ggg atc ata ttg gac     1507
172   Ser Leu Ser Trp Gln Glu Pro Glu His Pro Asn Gly Ile Ile Leu Asp
173         455                   460                   465
175   tac gag gtc aaa tac tat gaa aag cag gaa caa gaa aca agt tat acc     1555
176   Tyr Glu Val Lys Tyr Tyr Glu Lys Gln Glu Gln Glu Thr Ser Tyr Thr
177   470                   475                   480                   485
179   att ctg agg gca aga ggc aca aat gtt acc atc agt agc ctc aag cct     1603
180   Ile Leu Arg Ala Arg Gly Thr Asn Val Thr Ile Ser Ser Leu Lys Pro
181         490                   495                   500
183   gac act ata tac gta ttc caa atc cga gcc cga aca gcc gct gga tat     1651
184   Asp Thr Ile Tyr Val Phe Gln Ile Arg Ala Arg Thr Ala Ala Gly Tyr
185         505                   510                   515
187   ggg acg aac agc cgc aag ttt gag ttt gaa act agt cca gac tct ttc     1699
188   Gly Thr Asn Ser Arg Lys Phe Glu Phe Glu Thr Ser Pro Asp Ser Phe
189         520                   525                   530
191   tcc atc tct ggt gaa agt agc caa gtg gtc atg atc gcc att tca gcg     1747
192   Ser Ile Ser Gly Glu Ser Ser Gln Val Val Met Ile Ala Ile Ser Ala
193         535                   540                   545
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195   gca gta gca att att ctc ctc act gtt gtc atc tat gtt ttg att ggg    1795
196   Ala Val Ala Ile Ile Leu Leu Thr Val Val Ile Tyr Val Leu Ile Gly
197   550             555             560             565
199   agg ttc tgt ggc tat aag tca aaa cat ggg gca gat gaa aaa aga ctt    1843
200   Arg Phe Cys Gly Tyr Lys Ser Lys His Gly Ala Asp Glu Lys Arg Leu
201               570             575             580
203   cat ttt ggc aat ggg cat tta aaa ctt cca ggt ctc agg act tat gtt    1891
204   His Phe Gly Asn Gly His Leu Lys Leu Pro Gly Leu Arg Thr Tyr Val
205               585             590             595
207   gac cca cat aca tat gaa gac cct acc caa gct gtt cat gag ttt gcc    1939
208   Asp Pro His Thr Tyr Glu Asp Pro Thr Gln Ala Val His Glu Phe Ala
209               600             605             610
211   aag gaa ttg gat gcc acc aac ata tcc att gat aaa gtt gtt gga gca    1987
212   Lys Glu Leu Asp Ala Thr Asn Ile Ser Ile Asp Lys Val Val Gly Ala
213       615             620             625
215   ggt gaa ttt gga gag gtg tgc agt ggt cgc tta aaa ctt cct tca aaa    2035
216   Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Ser Lys
217   630             635             640             645
219   aaa gag att tca gtg gcc att aaa acc ctg aaa gtt ggc tac aca gaa    2083
220   Lys Glu Ile Ser Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu
221               650             655             660
223   aag cag agg aga gac ttc ctg gga gaa gca agc att atg gga cag ttt    2131
224   Lys Gln Arg Arg Asp Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe
225               665             670             675
227   gac cac ccc aat atc att cga ctg gaa gga gtt gtt acc aaa agt aag    2179
228   Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr Lys Ser Lys
229               680             685             690
231   cca gtt atg att gtc aca gaa tac atg gag aat ggt tcc ttg gat agt    2227
232   Pro Val Met Ile Val Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Ser
233       695             700             705
235   ttc cta cgt aaa cac gat gcc cag ttt act gtc att cag cta gtg ggg    2275
236   Phe Leu Arg Lys His Asp Ala Gln Phe Thr Val Ile Gln Leu Val Gly
237   710             715             720             725
239   atg ctt cga ggg ata gca tct ggc atg aag tac ctg tca gac atg ggc    2323
240   Met Leu Arg Gly Ile Ala Ser Gly Met Lys Tyr Leu Ser Asp Met Gly
241               730             735             740
243   tat gtt cac cga gac ctc gct gct cgg aac atc ttg atc aac agt aac    2371
244   Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Ile Asn Ser Asn
245               745             750             755
247   ttg gtg tgt aag gtt tct gat ttc gga ctt tcg cgt gtc ctg gag gat    2419
248   Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp
249           760             765             770
251   gac cca gaa gct gct tat aca aca aga gga ggg aag atc cca atc agg    2467
252   Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg
253       775             780             785
255   tgg aca tca cca gaa gct ata gcc tac cgc aag ttc acg tca gcc agc    2515
256   Trp Thr Ser Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala Ser
257   790             795             800             805
259   gat gta tgg agt tat ggg att gtt ctc tgg gag gtg atg tct tat gga    2563
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RAW SEQUENCE LISTING   DATE: 03/07/2002
PATENT APPLICATION: US/09/913,756   TIME: 18:40:43

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\03072002\I913756.raw

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260  Asp Val Trp Ser Tyr Gly Ile Val Leu Trp Glu Val Met Ser Tyr Gly
261              810              815              820
263  gag aga cca tac tgg gag atg tcc aat cag gat gta att aaa gct gta      2611
264  Glu Arg Pro Tyr Trp Glu Met Ser Asn Gln Asp Val Ile Lys Ala Val
265              825              830              835
267  gat gag ggc tat cga ctg cca ccc ccc atg gac tgc cca gct gcc ttg      2659
268  Asp Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ala Ala Leu
269              840              845              850
271  tat cag ctg atg ctg gac tgc tgg cag aaa gac agg aac aac aga ccc      2707
272  Tyr Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Asn Asn Arg Pro
273      855              860              865
275  aag ttt gag cag att gtt agt att ctg gac aag ctt atc cgg aat ccc      2755
276  Lys Phe Glu Gln Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Asn Pro
277  870              875              880              885
279  ggc agc ctg aag atc atc acc agt gca gcc gca agg cca tca aac ctt      2803
280  Gly Ser Leu Lys Ile Ile Thr Ser Ala Ala Ala Arg Pro Ser Asn Leu
281              890              895              900
283  ctt ctg gac caa agc aat gtg gat atc tct acc ttc cgc aca aca ggt      2851
284  Leu Leu Asp Gln Ser Asn Val Asp Ile Ser Thr Phe Arg Thr Thr Gly
285              905              910              915
287  gac tgg ctt aat ggt gtc cgg aca gca cac tgc aag gaa atc ttc acg      2899
288  Asp Trp Leu Asn Gly Val Arg Thr Ala His Cys Lys Glu Ile Phe Thr
289              920              925              930
291  ggc gtg gag tac agt tct tgt gac aca ata gcc aag att tcc aca gat      2947
292  Gly Val Glu Tyr Ser Ser Cys Asp Thr Ile Ala Lys Ile Ser Thr Asp
293      935              940              945
295  gac atg aaa aag gtt ggt gtc acc gtg gtt ggg cca cag aag aag atc      2995
296  Asp Met Lys Lys Val Gly Val Thr Val Val Gly Pro Gln Lys Lys Ile
297  950              955              960              965
299  atc agt agc att aaa gct cta gaa acg caa tca aag aat ggc cca gtt      3043
300  Ile Ser Ser Ile Lys Ala Leu Glu Thr Gln Ser Lys Asn Gly Pro Val
301              970              975              980
303  ccc gtg taa agcacgacgg aagtgcttct ggacggaagt ggtggctgtg              3092
304  Pro Val
307  gaaggcgtca agtcatcctg cagacagaca ataattctgg agatactggt ggaagtt       3149
309  <210> SEQ ID NO: 3
310  <211> LENGTH: 983
311  <212> TYPE: PRT
312  <213> ORGANISM: Homo sapiens
314  <400> SEQUENCE: 3
315  Met Asp Cys Gln Leu Ser Ile Leu Leu Leu Leu Ser Cys Ser Val Leu
316   1               5               10              15
317  Asp Ser Phe Gly Glu Leu Ile Pro Gln Pro Ser Asn Glu Val Asn Leu
318              20              25              30
319  Leu Asp Ser Lys Thr Ile Gln Gly Glu Leu Gly Trp Ile Ser Tyr Pro
320              35              40              45
321  Ser His Gly Trp Glu Glu Ile Ser Gly Val Asp Glu His Tyr Thr Pro
322      50              55              60
323  Ile Arg Thr Tyr Gln Val Cys Asn Val Met Asp His Ser Gln Asn Asn
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/07/2002
PATENT APPLICATION: US/09/913,756   TIME: 18:40:44

      Input Set : A:\PTO.AMC.txt
      Output Set: N:\CRF3\03072002\I913756.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 43